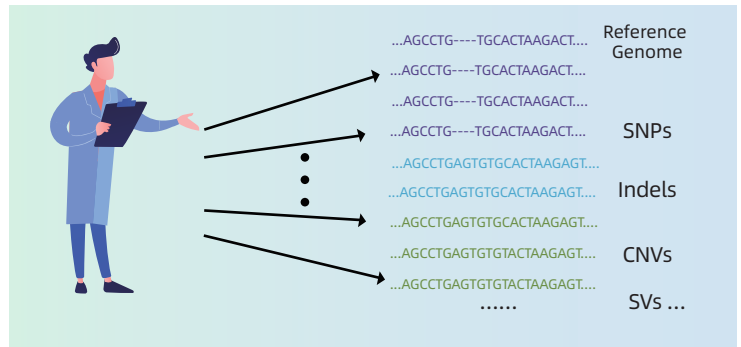
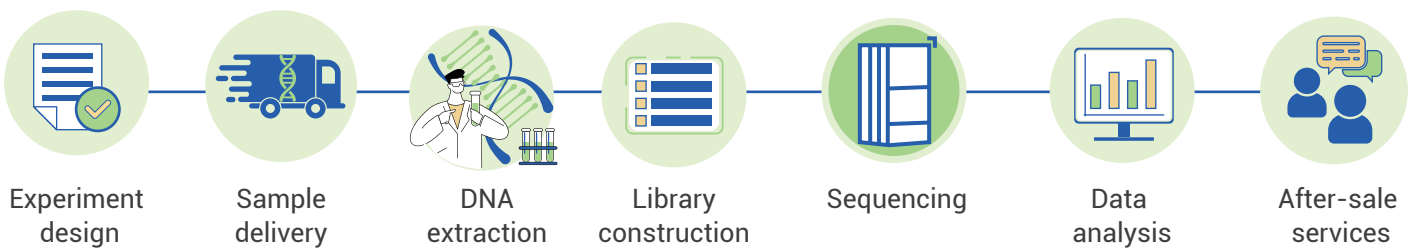


Human Whole Genome Sequencing

Whole genome sequencing delivers a comprehensive identification of small and large genetic variations across the entire human genome. It provides fundamental data resources for characterizing genetic markers associated with a variety of biological processes, which paves the way for new insights into diseases, cancers, population evolution, etc. BMKGENE offers human whole genome sequencing services on both next generation sequencing and third generation sequencing platforms for different scientific researches.



Service Workflow



Bioinformatics

- 1 Raw data quality control
- 2 Alignment with reference genome
- 3 SNP identification and annotation
- 4 Small InDel identification and annotation
- 5 SV, CNV identification and annotation (Long read sequencing or high depth)
- 6 Distribution of variations on genome
- 7 Functional annotation on variation (NR, SwissProt, GO, KEGG, COG, KOG, Pfam)



Service Advantages

- Detects multiple types of variations** Whole genome sequencing detects various types of variations, including SNP, InDel, SV, CNV, etc.
- Comprehensive genome information** Whole genome sequencing covers the entire genome, including exonic, intronic, non-coding, and intergenic regions, providing comprehensive variation identification.
- Diverse platform options** BMKGENE offers PacBio, Nanopore long read sequencing, and NGS Illumina/MGI sequencing.
- Rigorous quality control process** BMKGENE provides real-time quality control tracking for DNA extraction, library quality, sequencing base quality, sequence alignment, etc.
- Professional team** BMKGENE has dedicated teams with extensive experience in experimental design, data analysis, and customer service.

Service Specifications

Platform	Library	Sequencing Depth
Illumina NovaSeq MGI DNBSEQ-T7	PE150	≥ 30 X
Nanopore PromethION 48	8 kb	≥ 30 X
PacBio Revio	15 kb-HiFi	≥ 10 X

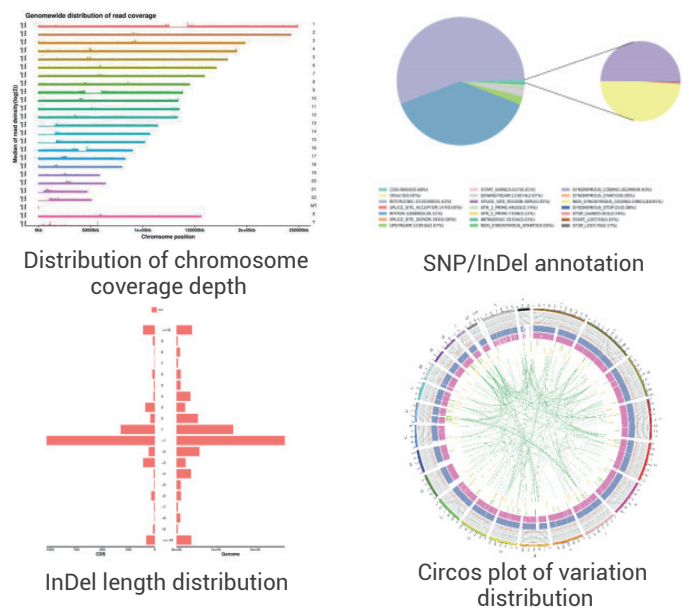
Sample Requirements

Platform	Conc. (ng/μL)	Amount (μg)	OD 260/280	Quality
Illumina/MGI PCR-FREE	≥ 1	≥ 0.03	-	Limited degradation and protein or RNA contamination
	≥ 40	≥ 0.5	-	
Nanopore	≥ 40	≥ 4	1.7-2.2	
PacBio	≥ 50	≥ 10	1.7-2.2	

Featured Publications

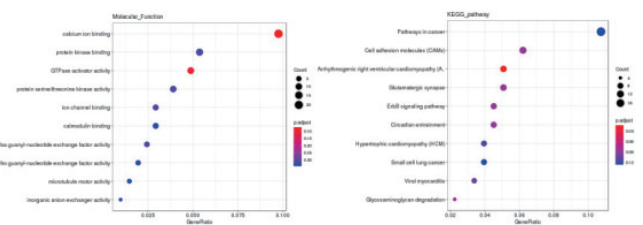


Demo Results



Total	Pathogenic	Likely pathogenic
795,299	18	528
VUS	Likely benign	Benign
296,436	178	498,139

Statistics of variant pathogenicity classification



GO/KEGG functional enrichment



Biomarker Technologies (BMKGENE)

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Global Locations

Germany United Kingdom United States China